**Amendments to the Specification:**

Please replace the paragraph on page 6, line 31 through page 7, line 12, with the following amended paragraph:

Like mouse RGL3 and other RasGEF molecules, RGL3 contains three functional domains. A RasGEFN domain is located close to the N-terminal end (amino acid sequence 64 – 198), a RasGEF domain is found at the center of the molecule (amino acid sequence 243 – 506) and a RA (Ras association) domain is found at the C-terminal end (613 – 699). ~~http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi~~National Center for Biotechnology Information (NCBI) conserved domain search website, Altschul *et al.*, Nucleic Acids Res., 25:3389-3402 (1997). The RasGEFN domain is identified in a subset of guanine nucleotide exchange factor for Ras-like small GTPases. Recent crystal structure of the RasGEFN domain shows that this domain is alpha-helical and plays a "purely structural role". Boriack-Sjodin et al, Nature 394, 337-343 (1998). The RasGEF domain may function as the prime site for guanine nucleotide binding and exchange and the RA is a putative binding site for RasGTP effectors. Shao *et al., J. Biol. Chem.* 275:26914-26924 (2000).

Please replace the paragraph on page 7, lines 13-25, with the following amended paragraph:

Other signatures of the newly isolated RGL3 protein were identified by searching the PROSITE database, (~~http://www.expasy.ch/tools/scnpsit1.html~~Expert Protein Analysis System (ExPASy) web site). These include one *N*-glycosylation sites (339-342), three cAMP- and cGMP-dependent protein kinase phosphorylation site (374-377, 517-520, 523-526), fourteen protein kinase C phosphorylation sites (30-32, 36-38, 63-65, 99-101, 170-172, 277-279, 290-292, 342-344, 372-374, 388-390, 495-497, 512-514, 559-561, and 591-593), nine casein kinase II phosphorylation sites (40-43, 221-224, 247-250, 256-259, 277-280, 388-391, 402-405, 540-543, and 635-638), and thirteen *N*-myristoylation sites (24-29, 169-174, 181-186, 273-278, 283-288, 286-291, 303-308, 307-312, 410-415, 425-430, 554-559, 568-573, and 700-705).

Please replace the paragraph on page 20, lines 3-15, with the following amended paragraph:

For purposes herein, percent identity of two nucleic acid sequences is determined using the procedure of Tatiana *et al.*, "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", *FEMS Microbiol Lett.* 174:247-250 (1999), which procedure is effectuated by the computer program BLAST 2 SEQUENCES, available online at ~~http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html~~the National Center for Biotechnology Information (NCBI) website. To assess percent identity of nucleic acids,

the BLASTN module of BLAST 2 SEQUENCES is used with default values of (i) reward for a match: 1; (ii) penalty for a mismatch: -2; (iii) open gap 5 and extension gap 2 penalties; (iv) gap X_dropoff 50 expect 10 word size 11 filter, and both sequences are entered in their entireties.

Please replace the paragraph on page 73, lines 19-25, with the following amended paragraph:

Bacterial cells can be rendered electrocompetent — that is, competent to take up exogenous DNA by electroporation — by various pre-pulse treatments; vectors are introduced by electroporation followed by subsequent outgrowth in selected media. An extensive series of protocols is provided online in Electroprotocols Online: Collection of Protocols for Gene Transfer (Bulletin #1029735, BioRad, Richmond, CA, USA) ~~(http://www.bio-rad.com/LifeScience/pdf/New_Gene_Pulser.pdf)~~.

Please replace the paragraph on page 74, line 28 through page 75, line 13, with the following amended paragraph:

For chemical transfection, DNA can be coprecipitated with $CaPO_4$ or introduced using liposomal and nonliposomal lipid-based agents. Commercial kits are available for $CaPO_4$ transfection (CalPhos™ Mammalian Transfection Kit, Clontech Laboratories, Palo Alto, CA, USA), and lipid-mediated transfection can be practiced using commercial reagents, such as LIPOFECTAMINE™ 2000, LIPOFECTAMINE™ Reagent,

CELLFECTIN® Reagent, and LIPOFECTIN® Reagent (Invitrogen, Carlsbad, CA, USA), DOTAP Liposomal Transfection Reagent, FuGENE 6, X-tremeGENE Q2, DOSPER, (Roche Molecular Biochemicals, Indianapolis, IN USA), Effectene™, PolyFect®, Superfect® (Qiagen, Inc., Valencia, CA, USA). Protocols for electroporating mammalian cells can be found online in Electroprotocols Online: Collection of Protocols for Gene Transfer (Bulletin #1029735, BioRad, Richmond, CA, USA) ~~(http://www.bio-rad.com/LifeScience/pdf/New_Gene_Pulser.pdf)~~. *See also*, Norton *et al.* (eds.), Gene Transfer Methods: Introducing DNA into Living Cells and Organisms, BioTechniques Books, Eaton Publishing Co. (2000) (ISBN 1-881299-34-1), incorporated herein by reference in its entirety.

Please replace the paragraph on page 76, line 28 through page 77, line 9, with the following amended paragraph:

For purposes herein, percent identity of two amino acid sequences is determined using the procedure of Tatiana *et al.*, "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", *FEMS Microbiol Lett.* 174:247-250 (1999), which procedure is effectuated by the computer program BLAST 2 SEQUENCES, available online at ~~http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html,~~the National Center for Biotechnology Information (NCBI) website. To assess percent identity of amino acid sequences, the BLASTP module of BLAST 2 SEQUENCES is used with default values of (i) BLOSUM62 matrix, Henikoff *et al.*, *Proc. Natl. Acad. Sci USA* 89(22):10915-9

(1992); (ii) open gap 11 and extension gap 1 penalties; and (iii) gap x_dropoff 50 expect 10 word size 3 filter, and both sequences are entered in their entireties.

Please replace the paragraph on page 129, lines 6-10, with the following amended paragraph:

Motif searches using Pfam (~~http://pfam.wustl.edu~~Washington University, St. Louis, web site), SMART (~~http://smart.embl- heidelberg.de~~European Molecular Biology Laboratory, Heidelberg, web site), and PROSITE pattern and profile databases (~~http://www.expasy.ch/prosite~~Expert Protein Analysis System (ExPASy) web site), identified several known domains shared with mouse RGL3 and other RasGEF proteins.

Please replace the paragraph on page 129, line 32 through page 130, line 13, with the following amended paragraph:

Like mouse RGL3 and other RasGEF molecules, RGL3 contains three functional domains. A RasGEFN domain is located close to the N-terminal end (amino acid sequence 64 – 198), a RasGEF domain is found at the center of the molecule (amino acid sequence 243 – 506) and a RA (Ras association) domain is found at the C-terminal end (613 – 699). ~~http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi~~National Center for Biotechnology Information (NCBI) conserved domain search website, Altschul *et al.*, Nucleic Acids Res., 25:3389-3402 (1997). The RasGEFN domain is identified in a subset of guanine nucleotide exchange factor for Ras-like small GTPases. Recent crystal

structure of the RasGEFN domain shows that this domain is alpha-helical and plays a "purely structural role". Boriack-Sjodin et al, Nature 394, 337-343 (1998). The RasGEF domain may function as the prime site for guanine nucleotide binding and exchange and the RA is a putative binding site for RasGTP effectors. Shao *et al., J. Biol. Chem.* 275:26914-26924 (2000).

Please replace the paragraph on page 130, lines 14-26, with the following amended paragraph:

Other signatures of the newly isolated RGL3 protein were identified by searching the PROSITE database, (~~http://www.expasy.ch/tools/scnpsit1.html~~Expert Protein Analysis System (ExPASy) web site). These include one *N*-glycosylation sites (339-342), three cAMP- and cGMP-dependent protein kinase phosphorylation site (374-377, 517-520, 523-526), fourteen protein kinase C phosphorylation sites (30-32, 36-38, 63-65, 99-101, 170-172, 277-279, 290-292, 342-344, 372-374, 388-390, 495-497, 512-514, 559-561, and 591-593), nine casein kinase II phosphorylation sites (40-43, 221-224, 247-250, 256-259, 277-280, 388-391, 402-405, 540-543, and 635-638), and thirteen *N*-myristoylation sites (24-29, 169-174, 181-186, 273-278, 283-288, 286-291, 303-308, 307-312, 410-415, 425-430, 554-559, 568-573, and 700-705).

Please replace the paragraph on page 131, lines 3-7, with the following amended paragraph:

Transcription factor binding sites were identified using a ~~web based program (http://motif.genome.ad.jp/)~~sequence motif search program (GenomeNet website, Kyoto University Bioinformatics Center), including binding sites for Lyf1 (49-57 and 365-373), CdxA (320-326, 611-617 and 623-629, with numbering according to SEQ ID NO: 29), amongst others.